

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/537,507  
Source: pc  
Date Processed by STIC: 3/9/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/537,507

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)         SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi)        SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                    Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,507

DATE: 03/09/2006

TIME: 12:36:38

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\03092006\J537507.raw

*see item 2 on  
Even summary  
sheet*

3 <110> APPLICANT: Aarhus Universitet  
5 <120> TITLE OF INVENTION: Method for determining predisposition to  
manifestation of immune system  
6 related diseases

8 &lt;130&gt; FILE REFERENCE: P 706 DK 02

C--&gt; 10 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/537,507

C--&gt; 10 &lt;141&gt; CURRENT FILING DATE: 2005-06-03

10 &lt;160&gt; NUMBER OF SEQ ID NOS: 8

12 &lt;170&gt; SOFTWARE: PatentIn version 3.1

14 &lt;210&gt; SEQ ID NO: 1

15 &lt;211&gt; LENGTH: 671

16 &lt;212&gt; TYPE: PRT

17 &lt;213&gt; ORGANISM: Homo sapiens; mature MASP-2

19 &lt;400&gt; SEQUENCE: 1

21 Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala

22 1 5 10 15

25 Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp

26 20 25 30

29 Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His

30 35 40 45

33 Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu

34 50 55 60

37 Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr

38 65 70 75 80

41 Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser

42 85 90 95

45 Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe

46 100 105 110

49 Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln

50 115 120 125

53 Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His

54 130 135 140

57 Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg

58 145 150 155 160

61 Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln

62 165 170 175

65 Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys

66 180 185 190

69 Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val

70 195 200 205

73 Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr

74 210 215 220

77 Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His

78 225 230 235 240

**Does Not Comply  
Corrected Diskette Needed**

*pp 3-5*

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Input Set : A:\PTO.KD.txt

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81 Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
82                245                250                255
85 Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
86                260                265                270
89 Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
90                275                280                285
93 Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
94                290                295                300
97 Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
98 305                310                315                320
101 Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
102                325                330                335
105 Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
106                340                345                350
109 Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
110                355                360                365
113 Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
114                370                375                380
117 Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
118 385                390                395                400
121 Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
122                405                410                415
125 Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
126                420                425                430
129 Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
130                435                440                445
133 Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
134                450                455                460
137 Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
138 465                470                475                480
141 Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
142                485                490                495
145 Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
146                500                505                510
149 Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
150                515                520                525
153 Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
154                530                535                540
157 Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
158 545                550                555                560
161 Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
162                565                570                575
165 Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
166                580                585                590
169 Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
170                595                600                605
173 Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
174                610                615                620
177 Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp

```



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```

270 tgtccctacg actttctcaa gattcaaaaca gacagagaag aacatggccc attctgtggg      780
272 aagacattgc cccacaggat tgaaacaaaa agcaacacgg tgaccatcac ctttgtcaca      840
274 gatgaatcag gagaccacac aggctggaag atccactaca cgagcacagc gcagccttgc      900
276 ccttatccga tggcgccacc taatggccac gtttcacctg tgcaagccaa atacatcctg      960
278 aaagacagct tctccatctt ttgcgagact ggctatgagc ttctgcaagg tcacttgccc     1020
280 ctgaaatcct ttactgcagt ttgtcagaaa gatggatctt gggaccggcc aatgcccgcg     1080
282 tgcagcattg ttgactgtgg ccctcctgat gatctaccca gtggccgagt ggagtacatc     1140
284 acaggctctg gagtgaccac ctacaaagct gtgattcagt acagctgtga agagaccttc     1200
286 tacacaatga aagtgaatga tggtaaatat gtgtgtgagg ctgatggatt ctggacgagc     1260
288 tccaaaggag aaaaatcact ccagctctgt gagcctgttt gtggactatc agcccgacac     1320
290 acaggagggc gtatatatgg agggcaaaag gcaaaacctg gtgattttcc ttggcaagtc     1380
292 ctgatattag gtggaaccac agcagcaggt gcacttttat atgacaactg ggtcctaaca     1440
294 gctgctcatg ccgtctatga gcaaaaacat gatgcatccg ccctggacat tcgaatgggc     1500
296 accctgaaaa gactatcacc tcattataca caagcctggt ctgaagctgt ttttatacat     1560
298 gaaggttata ctcatgatgc tggctttgac aatgacatag cactgattaa attgaataac     1620
300 aaagttgtaa tcaatagcaa catcacgcct atttgtctgc caagaaaaga agctgaatcc     1680
302 tttatgagga cagatgacat tggaaactgca tctggatggg gattaaccca aaggggtttt     1740
304 cttgctagaa atctaatagt tgtcgacata ccgattgttg accatcaaaa atgtactgct     1800
306 gcatatgaaa agccacccta tccaagggga agtgtaactg ctaacatgct ttgtgctggc     1860
308 ttagaaagtg ggggcaagga cagctgcaga ggtgacagcg gaggggcact ggtgtttcta     1920
310 gatagtgaag cagagaggtg gtttgtggga ggaatagtgt cctgggggttc catgaattgt     1980
312 ggggaagcag gtcagtatgg agtctacaca aaagttatta actatatccc ctggatcgag     2040
314 aacataatta gtgattttta a                                     2061
317 <210> SEQ ID NO: 4
318 <211> LENGTH: 558
319 <212> TYPE: DNA
320 <213> ORGANISM: cdNA MAP-19 same env
322 <400> SEQUENCE: 4
323 atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg      60
325 aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc     120
327 aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac     180
329 ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc     240
331 tcggggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcggggc     300
333 cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac     360
335 tactccaacg agaagccgtt cacgggggtc gaggccttct atgcagccga ggacattgac     420
337 gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg     480
339 ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc     540
341 tcagagcaga gcctctag                                     558
344 <210> SEQ ID NO: 5
345 <211> LENGTH: 21
346 <212> TYPE: DNA
347 <213> ORGANISM: upper PCR primer
349 <400> SEQUENCE: 5
350 gcgagtacga cttcgtcaag g                                     21
353 <210> SEQ ID NO: 6
354 <211> LENGTH: 21
355 <212> TYPE: DNA
356 <213> ORGANISM: lower PCR primer
358 <400> SEQUENCE: 6

```

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Input Set : A:\PTO.KD.txt

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359 ctcggctgca tagaaggcct c 21  
362 <210> SEQ ID NO: 7  
363 <211> LENGTH: 21  
364 <212> TYPE: DNA  
365 <213> ORGANISM: upper PCR primer  
367 <400> SEQUENCE: 7  
368 ccagaccttt ggaaagtttag c 21  
371 <210> SEQ ID NO: 8  
372 <211> LENGTH: 21  
373 <212> TYPE: DNA  
374 <213> ORGANISM: lower PCR primer  
376 <400> SEQUENCE: 8  
377 ggctcaagtt ccaagtattg c 21

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/537,507

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Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\03092006\J537507.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date